

[illegible]

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=MUSCLE;
RA Laplace C., Costet P.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; X74510; CA452616.1; -.
DR EMBL; AF240002; AA64470.1; -.
DR INTERPRO; IPR001993; -.
DR INTERPRO; IPR002067; -.
DR INTERPRO; IPR002113; -.
DR PFAM; PF00153; mito_carr; 1.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00927; ADPTRNSLASE.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KM Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

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	Query Match	91.9%;	Score 1418;	DB 11;	Length 298;	
	Best Local Similarity	88.9%;	Pred. No. 7.2e-122;			
	Matches 265;	Conservative 19;	Mismatches 14;	Indels 0;	Gaps 0;	
Oy	1 MTEQAISFAKDFLAGGIAAISKTAVAPIERYVKLLQVOHASKOJIAADKYKIVDCITVR	60				
Dd	1 : ::: ::: ::: ::: ::: ::: ::: :::	60				
	1 :MDDQALSFELKFDFLAGGIAAAVSKTAVAPIERYKLLQVOHASKOJISAERKKGIIDCVLR	60				
Oy	61 IPKEGVLSFPMGNLANIYIRFPOTALNPAFDKXKOYFLGVDYDHPTQFWRFAGNLASG	120				
Dd	61 ::: ::: ::: ::: ::: ::: ::: :::	120				
	61 IPKEGGFSFPMRGNIANVIRFTPTOLNPAFKDKKQFLFGVDYRHKQPFWRFFAGNLASG	120				
Oy	121 GAAGATSLCFEYVPILDFAARTLAAADVKGSGTEREFRLGDCLVTKITSDGINGLYOGFSVS	180				
Dd	121 ::: ::: ::: ::: ::: ::: ::: :::	180				
	121 GAAGATSLCFEYVPILDEAFARTRLAADVKGSSQSEREFNGLDGCGLTKIKPSDGLKGLYOGFSVS	180				
Oy	181 VGGIIITRAATRVGVDTAKGMPLPDRKNHIYVSMIACTVATAVAGVSYPRDTPARRMM	240				
Dd	181 ::: ::: ::: ::: ::: ::: ::: :::	240				
	181 VGGIIITRAATRVGVDTAKGMPLPDRKNHIIYSWIAOSVATAVALVSYPRDTPARRMM	240				
Oy	241 GSGRGADIMVTGTADCNRKIFPDGCGKAFFKGAMSNVLRGMGAFVYLVDLKKVI	298				
Dd	241 ::: ::: ::: ::: ::: ::: ::: :::	298				
	241 GSGRGADIMVTGTIDCNRKIADKGANAFFKGAMSNVLRGMGAFVLYLDELRIKVY	298				
RESULT	4					
ID	09PRH1	PRELIMINARY;	PRT;	298 AA.		
AC	09PRH1:					
DT	01-MAY-2000 (TREMBLrel..13, Created)					
DT	01-May-2000 (TREMBLrel..13, Last sequence update)					
DT	01-JUN-2000 (TREMBLrel..14, Last annotation update)					
DE	ADP/AFP TRANSLOCASE.					
OS	Rana rugosa (Frog) .					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranae; Rana.					
OX	NCBI_TaxId=8410;					
RN	[1]					
RA	SEQUENCE FROM N.A.					
RA	Miyura I., Ohnishi H., Nakamura M., Ichikawa Y., Saitoh K.;					
RT	"The origin and differentiation of the heteromorphic sex chromosomes					
RT	Z., W., X., and Y in the frog Rana rugosa, inferred from the sequences of					


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RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
DR EMBL: AB008463; BAA36513.1; -
DR EMBL: AB008456; BAA36506.1; -
DR EMBL: AB008461; BAA36511.1; -
DR EMBL: AB008462; BAA36512.1; -
DR INTERPRO: IPR001993; -
DR INTERPRO: IPR002030; -
DR INTERPRO: IPR002067; -
DR INTERPRO: IPR002113; -
DR PFAM: PF00153; mito.carr. 1.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 91.3%; Score 1409; DB 13; Length 298;
Best Local Similarity 88.6%; Pred. No. 4.8e-121;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEOAISFAKDFLAGGIAAISTAVAPIERVKLLLOVQHASKOIAADKOYKGIYDCIVR 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTDAAISFAKDFLAGGVAALISKTAVAPIERVKLLLOVQHASKOITADKOYKGIIMDCVVR 60

QY 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDPKHQFMRYFAGNLASG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDPKHQFMRYFAGNLASG 120

QY 121 GAAGATSLCFYYPIDFATRLAADVGSSTEREFGGLDCLVKITKSDGIRGLYOGFSVS 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYYPIDFATRLAADVGSSTEREFGGLDCLVKITKSDGIRGLYOGFSVS 180

QY 181 VOGIIITYAAAFGVYDPAKGLPDPKNTHIYVSMIAQTVTAAGVVSYPEDTVRRMM 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VOGIIITYAAAFGVYDPAKGLPDPKNTHIYVSMIAQTVTAAGVVSYPEDTVRRMM 240

QY 241 QSGRKGADIMYTGVDCKRIFRDEGKAFKFGKAMSNVLRMGCAFVLVLYDELKKVI 298
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGADIMYTGVDCKRIFRDEGKAFKFGKAMSNVLRMGCAFVLVLYDELKKVI 298

RESULT 5
Q9PRH2 PRELIMINARY; PRT; 298 AA.
AC Q9PRH2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
   Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
   a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
DR EMBL: AB008460; BAA36510.1; -
DR EMBL: AB008458; BAA36508.1; -
DR EMBL: AB008459; BAA36509.1; -
DR INTERPRO: IPR001993; -
DR INTERPRO: IPR002030; -
DR INTERPRO: IPR002067; -
DR INTERPRO: IPR002113; -
DR PFAM: PF00153; mito.carr. 1.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.

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DR PROSITE: PS00215; MITOCH_CARRIER. 3.
SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 91.1%; Score 1406; DB 13; Length 298;
Best Local Similarity 88.3%; Pred. No. 9e-121;
Matches 263; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEOAISFAKDFLAGGIAAISTAVAPIERVKLLLOVQHASKOIAADKOYKGIYDCIVR 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTDAAISFAKDFLAGGVAALISKTAVAPIERVKLLLOVQHASKOITADKOYKGIIMDCVVR 60

QY 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDPKHQFMRYFAGNLASG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDPKHQFMRYFAGNLASG 120

QY 121 GAAGATSLCFYYPIDFATRLAADVGSSTEREFGGLDCLVKITKSDGIRGLYOGFSVS 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYYPIDFATRLAADVGSSTEREFGGLDCLVKITKSDGIRGLYOGFSVS 180

QY 181 VOGIIITYAAAFGVYDPAKGLPDPKNTHIYVSMIAQTVTAAGVVSYPEDTVRRMM 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VOGIIITYAAAFGVYDPAKGLPDPKNTHIYVSMIAQTVTAAGVVSYPEDTVRRMM 240

QY 241 QSGRKGADIMYTGVDCKRIFRDEGKAFKFGKAMSNVLRMGCAFVLVLYDELKKVI 298
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGADIMYTGVDCKRIFRDEGKAFKFGKAMSNVLRMGCAFVLVLYDELKKVI 298

RESULT 6
Q9YIC4 PRELIMINARY; PRT; 298 AA.
AC Q9YIC4;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
   Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
   a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
   INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008457; BAA36507.1; -
DR INTERPRO: IPR001993; -
DR INTERPRO: IPR002030; -
DR INTERPRO: IPR002067; -
DR INTERPRO: IPR002113; -
DR PFAM: PF00153; mito.carr. 1.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 90.9%; Score 1402; DB 13; Length 298;
Best Local Similarity 87.9%; Pred. No. 2.1e-120;
Matches 262; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEOAISFAKDFLAGGIAAISTAVAPIERVKLLLOVQHASKOIAADKOYKGIYDCIVR 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTDAAISFAKDFLAGGVAALISKTAVAPIERVKLLLOVQHASKOITADKOYKGIIMDCVVR 60

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Oy 61 IPKEGVLSFPMGNLANVIRYPTQALNFAFKDKYKQIFLGVGDKHTQFMRYFAGNLASG 120
Db 61 IPKEGVLSFPMGNLANVIRYPTQALNFAFKDKYKQIFLGVGDKHTQFMRYFAGNLASG 120
Oy 121 GAAGATSLCFYVPLDPAFTRLAADVGSKGTREPRGLDCLVTKTKSDGIRGLYOGFSVS 180
Db 121 GAAGATSLCFYVPLDPAFTRLAADVGSKGTREPRGLDCLVTKTKSDGIRGLYOGFSVS 180
Oy 181 VGGIIYRAAFYGVYDTAKGMLPDPKNTNHYVSMWIAQTVAVAGVSPEDTVRRMM 240
Db 181 VGGIIYRAAFYGVYDTAKGMLPDPKNTNHYVSMWIAQTVAVAGVSPEDTVRRMM 240
Oy 241 QSRKGADIMYTGIVDCWRIKIFRDEGKAFFKAGMSNVLRGSGAFVLYLDELKVI 238
Db 241 QSRKGADIMYTGIVDCWRIKIFRDEGKAFFKAGMSNVLRGSGAFVLYLDELKVI 238
Oy 241 QSRKGADIMYTGIVDCWRIKIFRDEGKAFFKAGMSNVLRGSGAFVLYLDELKVI 238
Db 241 QSRKGADIMYTGIVDCWRIKIFRDEGKAFFKAGMSNVLRGSGAFVLYLDELKVI 238

RESULT 7
ID 091336 PRELIMINARY; PRT; 317 AA.
AC 091336;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana sylvatica (wood frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
OX NCBI_TaxID=45438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=97398141; PubMed=9256066;
RA Cai O., Greenway S.C., Storey K.B.;
RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
in wood frogs under freezing stress.";
RL Biochim. Biophys. Acta 1353:69-78(1997).
RN [2]
RP REVISIONS.
RA Cai O., Storey K.B.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1 INNER MEMBRANE (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: U04832; AAA97882.2;
DR INTERPRO: IPR001993;
DR INTERPRO: IPR002067;
DR INTERPRO: IPR002113;
DR PRAM: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KM Mitochondrion: Repeat: Transmembrane: Transport.
SQ SEQUENCE 317 AA; 35005 MW; 5F66E7ED8D5CEB72 CRC64;

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Query Match 81.6%; Score 1259; DB 13; Length 317;
Best Local Similarity 86.8%; Pred. No. 2.8e-107;
Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

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Oy 1 MTEQAISFADKFLAGIAAISKTAVPRIEYKLLLOVHASKOIAADKQYKGIIVDCIVR 60
Db 1 MTEQAISFADKFLAGIAAISKTAVPRIEYKLLLOVHASKOIAADKQYKGIIVDCIVR 60
Oy 61 IPKQGVLSFPMGNLANVIRYPTQALNFAFKDKYKQIFLGVGDKHTQFMRYFAGNLASG 120
Db 61 IPKQGVLSFPMGNLANVIRYPTQALNFAFKDKYKQIFLGVGDKHTQFMRYFAGNLASG 120
Oy 121 GAAGATSLCFYVPLDPAFTRLAADVGSKGTREPRGLDCLVTKTKSDGIRGLYOGFSVS 180
Db 121 GAAGATSLCFYVPLDPAFTRLAADVGSKGTREPRGLDCLVTKTKSDGIRGLYOGFSVS 180
Oy 121 GAAGATSLCFYVPLDPAFTRLAADVGSKGTREPRGLDCLVTKTKSDGIRGLYOGFSVS 180
Db 121 GAAGATSLCFYVPLDPAFTRLAADVGSKGTREPRGLDCLVTKTKSDGIRGLYOGFSVS 180

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Oy 181 VGGIIYRAAFYGVYDTAKGMLPDPKNTNHYVSMWIAQTVAVAGVSPEDTVRRMM 240
Db 181 VGGIIYRAAFYGVYDTAKGMLPDPKNTNHYVSMWIAQTVAVAGVSPEDTVRRMM 240
Oy 241 QSRKGADIMYTGIVDCWRIKIFRDEGKAFFK 272
Db 241 QSRKGADIMYTGIVDCWRIKIFRDEGKAFFR 272
Oy 241 QSRKGADIMYTGIVDCWRIKIFRDEGKAFFK 272
Db 241 QSRKGADIMYTGIVDCWRIKIFRDEGKAFFR 272

RESULT 8
ID 09VZ70 PRELIMINARY; PRT; 299 AA.
AC 09VZ70;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE SESB PROTEIN.
GN SESB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Burdick K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Jatala M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003484; AF47957.1;
DR FLYBASE: FBgn0003360; seSB.
DR INTERPRO: IPR001993;
DR INTERPRO: IPR002067;
DR INTERPRO: IPR002113;
DR PRAM: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.

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DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 299 AA; 32909 MW; D51F3E2A70BD59E8 CRC64;

Query Match	81.3%	Score 1254.5	DB 5	length 299
Best Local Similarity	80.6%	Pred. No. 6.7e-107		
Matches 237	Conservative 23	Mismatches 33	Indels 1	Gaps 1

[illegible]

RESULT	9	
ID	09NHMS	
AC	09NHMS	PRELIMINARY;
DT	01-OCT-2000 (Tremblrel. 15, Created)	PRT; 300 AA.
DT	01-OCT-2000 (Tremblrel. 15, last sequence update)	
DT	01-OCT-2000 (Tremblrel. 15, last annotation update)	
DE	ADP/ATP TRANSLOCASE.	
OS	Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Cecidozoidea; Calliphoridae; Lucilia.	
OX	NCBI_TaxID=7375;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=SS MAL SEEKING;	
RA	Chen Z., Fair J.A., Batterham P.;	
RT	"A cDNA clone encoding the ADP/ATP translocase of <i>Lucilia cuprina</i> ."	
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AF118587; AAF32322.1;	
SQ	SEQUENCE 300 AA; 33036 MW; 5459DFDEA0E2E742 CRC64;	

Query Match	80.1%	Score 1235.5	DB 5	Length 300
Best Local Similarity	79.5%	Pred. No. 3.7e-105		
Matches 233	Conservative 24	Mismatches 35	Indels 1	Gaps 1

Qy	I S F K P D I A G I A A I S K T N A P I E R X K L L O V H A S K O J A A M D Q Y C I D T Y I R I K E Q	65
Db	L G F V K D P A G I S I A A V S K T A A P I E R K L L O V H I S K I S P D Q Y G M I D C F R I P K E Q	68
Qy	G V L S F W R K G N L A N V R Y E P T Q A L N F A F K D K Y K Q I F L G S V D K H T O F W R Y F A G N L A S G A A G A	125
	: :	
Db	G F A S Y R G N M A N A N V I R Y P P T Q A L N F A P K D K Y K Q V F L G V D K N T O G W R Y F L N L A S G A A G A	128
Qy	T S L C F V Y P L D P A R I R L A A D V G K S G T E R E B P R G L D C L Y K I T K S D S I R G L Y O G F S V S V G I I	185
	: :	
Db	T S L C F V Y P L D P A R I R L A A D V G K G - Q R E P F G L G N C L A K I R S D S L V D L Y R K G F V S V G I I	187
Qy	I Y R A A Y E G V Y T A K G M L P D P K N T H I I V S M A I Q A V T V A G V S Y P F T V R R M M O S G R K	245
Db	I Y R A A Y E G V Y T A R G M L P D P K N T I I Y I S M A I Q A V V T V A G I V S Y P F T V R R M M O S G R K	247
Qy	G A D I M I T G T V D C M K R I I R D E G G K A F F E G G A S N V L R G M G A F V L V L Y D E L K V I	298

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Db      248 ATEIYKNLHCWATIAKQEGTGAFFKGAFSNVLRGTGAFVLVLYDEIKKL 300
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RESULT	10			
044093				
ID	044093	PRELIMINARY:	PRT:	288 AA.
AC	044093;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	ADP/ATP TRANSLOCASE (FRAGMENT).			
GN	SESB.			
OS	Drosophila pseudoobscura (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephyridioidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7237;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	zeng L.-W., Comerón J.M., Chen B., Kreitman M.;			
RL	Genetica 0:0-0(1997).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL			
CC	INNER MEMBRANE (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
DR	EMBL: AF025798; AAB87883.1; -			
DR	EMBLBASE: EFGM0023292; Dpse\sesb.			
DR	INTERPRO: IPR001993; -			
DR	INTERPRO: IPR002067; -			
DR	INTERPRO: IPR002113; -			
DR	PFAM: pf00153; mito_carr; 1.			
DR	PRINTS: PR00926; MITOCARRIER.			
DR	PRINTS: PR00927; ADPTRNSLCASE.			
DR	PROSITE: PS00215; MITOCH CARRIER. 3.			
FT	mitochondrion: Repeat: Transmembrane; Transport.			
KW	NON_TER	288	288	
SEQUENCE	288 AA; 31725 MW; 052B0CC005043650 CRC64;			

Query Match	77.0%	Score 1187.5	DB 5	length 288
Best Local Similarity	80.7%	Pred. No. 8.6e-101		
Matches 230	Conservative 19	Mismatches 33	Indels 3	Gaps 3

QY	5	AIIFAKDDLAGGIAAASIKSTVAPPERKLLLOYHNSKQIAAOKYKGVDCIVRIPKE	64
Db	7	AIGFYKDDAAGGISAASKTAVAPERKLLLOYHNSKQISPDQIKGVHDCITRIPKE	66
QY	65	QGVLSFWGKGLANVIRYEPYALNFAFKDKYKOIIFLGVDNHTQFWRYEAGNLAGGAAG	122
Db	67	QGFSEFWGKGLANVIRYEPYALNFAFKDKYKOVYFLGVDNTPQFWRYEAGNLAGGAAG	126
QY	125	ATSLCFVYPLDFAFTRILADYKSGTGEREPFLGIDCLYIKRSGDITGLYGGFASVQGI	184
Db	127	ATSLCFVYPLDFAFTRILADYKSGG - QNEPFLGIDCLYIKRSGDITGLYGGFASVQGI	188
QY	185	IIRAYAGVYDTAKGMLPDKRNTIHVVSMIACTVTAAVAGVSYPEDTVRRMMMSGR	244
Db	186	IIRAYAGVYDTAKR - MLPDKRNTPIYSMAIAOAVTVAIVSYPEDTVRRMMMSGR	244
QY	245	KGADIMYGTGVDCKRKIFRDEGGKAFFGASNVILRGGGAFVILV	289
Db	245	KATELIIVANTLHCMTATIAKOE - GSAFFFGASNVILRGGGAFVILV	288

RESULT	11	
04094		
04094	PRELIMINARY;	PRT: 288 AA.
AC 04094:		
DT 01-JUN-1998	(TREMBLrel 06, Created)	
DT 01-JUN-1998	(TREMBLrel 05, Last sequence update)	
DT 01-OCT-2000	(TREMBLrel 15, Last annotation update)	
DE ADP/ATP TRANSLOCASE (FRAGMENT).		
NN SESB.		

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Idegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson J.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Renner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OREGON-R;
 RL Zhang Y.Q., Davis A.W., Roote J., Ashburner M.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003484; AAF47956.1;
 DR FLYBASE: CA71629.1;
 DR FLYBASE: FBgn0025111; Ant2.
 DR INTERPRO: IPR001993;
 DR INTERPRO: IPR002067;
 DR INTERPRO: IPR002113;
 DR PFAM: PF00133; mito_carr; 1.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH CARRIER; UNKNOWN 2.
 SO SEQUENCE 307 AA; 33744 MW; 3D6B3DFD82061C0C CRC64;

Query Match 73.7%; Score 1137.5; DB 5; Length 307;
 Best Local Similarity 74.8%; Pred. No. 3.6e-96;
 Matches 217; Conservative 26; Mismatches 46; Indels 1; Gaps 1;
 Oy 7 SPADFLAGGIAAISKTAAPVPIERVKLLQVOHASKOIAADKQYGIYDCIVIRPKEGG 66
 Db 17 SFLDPMFGVSAIAKTAAPVPIERVKLLQVOHASKOIAADKQYGIYDCIVIRPKEGG 76
 Oy 67 VLSFMRGLANVIRFPQALNFAFKDKYKQIFLGVDKHFQFMRYFAGNLSGGAAGAT 126
 Db 77 FSSFMRLANVIRFPQALNFAFKDKYKQIFLGVDKHFQFMRYFAGNLSGGAAGAT 136
 Oy 127 SLCEFYPLDFARTRLAADVGKSGTEREFGGLDCLVYIKTSKDGIRGLYOGFSVVOGII 186
 Db 137 SLCEFYPLDFARTRLAADVGKSGTEREFGGLDCLVYIKTSKDGIRGLYOGFSVVOGII 195
 Oy 187 YRAAFGYDPAKGM-LPDKNTHIVSMIAQVTAAGVVSYPEDTVRRMMQSGRKG 246
 Db 196 YRAAFGYDPAKGM-LPDKNTHIVSMIAQVTAAGVVSYPEDTVRRMMQSGRKG 255
 Oy 247 ADIMVTGVDDMRKIFRDEGKAPFGKASNVLRGMSGAFVLYLDEKKY 296
 Db 256 SEMVYKNTAHKLVYIAKOGIGAFKGLSNIRGTGALVALYIDEMK 305
 RESULT 14
 ID 021103 PRELIMINARY; PRT: 313 AA.
 AC 021103.
 DT 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE K01H12.2 PROTEIN.
 GN K01H12.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mcmurray A.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Ljotting J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*."
 RL Nature 368:37-38(1994).
 CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: Z68218; CA92472.1;
 DR EMBL: Z68218; CA92472.1;
 DR INTERPRO: IPR001993;
 DR INTERPRO: IPR002067;
 DR INTERPRO: IPR002113;
 DR PFAM: PF00133; mito_carr; 1.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH CARRIER; 3.
 KW Mitochondrion; Repeat; Transmembrane; Transport.
 SO SEQUENCE 313 AA; 34384 MW; D1E455DDB463C984 CRC64;

Query Match 67.5%; Score 1041; DB 5; Length 313;
 Best Local Similarity 70.9%; Pred. No. 2.5e-87;
 Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;
 Oy 8 FAKDFLAGGIAAISKTAAPVPIERVKLLQVOHASKOIAADKQYGIYDCIVIRPKEGG 67
 Db 25 FLIDLASGCTAAAVSKTAAPVPIERVKLLQVOHASKOIAADKQYGIYDCIVIRPKEGG 84
 Oy 68 LSPFMRLANVIRFPQALNFAFKDKYKQIFLGVDKHFQFMRYFAGNLSGGAAGAT 127
 Db 85 AALMRGLANVIRFPQALNFAFKDKYKQIFLGVDKHFQFMRYFAGNLSGGAAGAT 144
 Oy 128 LCFYVPLDFARTRLAADVGKSGTEREFGGLDCLVYIKTSKDGIRGLYOGFSVVOGII 187
 Db 145 LCFYVPLDFARTRLAADVGKSGTEREFGGLDCLVYIKTSKDGIRGLYOGFSVVOGII 203
 Oy 188 RAAFGYDPAKGM-LPDKNTHIVSMIAQVTAAGVVSYPEDTVRRMMQSGRKG 246
 Db 204 RAAFGYDPAKGM-LPDKNTHIVSMIAQVTAAGVVSYPEDTVRRMMQSGRKG 262
 Oy 247 ADIMVTGVDDMRKIFRDEGKAPFGKASNVLRGMSGAFVLYLDEKKY 298
 Db 263 -DVLKNTLDAVKITIKNEGMSAMFKGALSNVFGTSGALVALYIDELQKFI 313
 RESULT 15
 ID P91410 PRELIMINARY; PRT: 313 AA.
 AC P91410.
 DT 01-MAY-1997 (Tremblrel. 03, Created)

Search completed: April 29, 2001, 11:38:54
 Job time: 154 sec

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DT 01-MAY-1997 (TReMBLrel. 03, last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, last annotation update)
DE SIMILAR TO ADP/ATP TRANSLOCASE.
GN TOB11.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peleodermidae; Caenorhabditis.
OX NCBI_TaxID=6239.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RX MEDLINE=94150718; PubMed=7906398.
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sprat J., Woldman P.,
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RA Geisel C., Stellyes L.
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RA Waterston R.
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY).
CC CC EMBL: U80931; AAB38001.1; -.
DR INTERPRO: IPR001993; -.
DR INTERPRO: IPR002067; -.
DR INTERPRO: IPR002113; -.
DR PRAM: PF00153; mito_carrf.1.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLOCASE.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KM Mitochondrion: Repeat: Transmembrane: Transport.
SQ SEQUENCE 313 AA; 34356 MW; CF07C473A719CCB6 CRC64;

Query Match 67.3%; Score 1039; DB 5; Length 313;
Best Local Similarity 70.9%; Pred. No. 3.9e-87;
Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

QY 8 FAKDLGAGTAAIAISKTAAPVIERVKLLLOVQHASKOIADKQYGIYDCIVRIPEKQGV 67
DB 25 FLIDLASGCTAAAVSKTAAPVIERVKLLLOVQDASLTIAADKRYKGIYDVLRVPEKQGY 84
QY 68 LSPFRGNLANVIRYEPQALNFAFKDKYKQIEFGVDKHKQFMRYEPAGNLSGGAAGATS 127
DB 85 AALMRGNLANVIRYEPQALNFAFKDKYKQIEFGVDKHKQFMRYEPAGNLSGGAAGATS 144
QY 128 LCFVYPLDFAFTRLAADVGSKSTEREFRGLDCLVKTFSKGIKGLXQGFVSVOGIIIT 187
DB 145 LCFVYPLDFAFTRLAADVGSKSTEREFRGLDCLVKTFSKGIKGLXQGFVSVOGIIIT 203
QY 188 RAAFGYVDTAKGML-PDPKNTIIVSMMIAQVTAAGVSYSPFTVRRMMQSGRKG 246
DB 204 RAAFGYVDTAKGML-PDPKNTIIVSMMIAQVTAAGVSYSPFTVRRMMQSGRKG 262
QY 247 ADIWTGTVDQWRKIIFDEGSKAFKGCAMSVVLGGMGAPVLYLXDELKVI 298
DB 263 -DVLYKNTLDCAVKTIINSGSAMFKGALSINVFRTGALVLAITYDEIQKFI 313

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 29, 2001, 11:37:06 ; Search time 9.46 Seconds

(without alignments)
1079,084 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543
Sequence: 1 MTEQALSFADKFLAGGIAAA.....LRMGCAFVLYVDELKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1543	100.0	298 1	ADT3_HUMAN
2	1512	98.0	298 1	ADT3_BOVIN
3	1463	94.8	298 1	ADT2_HUMAN
4	1451	94.0	298 1	ADT2_RAT
5	1445	93.6	298 1	ADT2_MOUSE
6	1424	92.3	298 1	ADT1_RAT
7	1417	91.8	297 1	ADT1_BOVIN
8	1412	91.5	298 1	ADT1_MOUSE
9	1409	91.3	298 1	ADT1_HUMAN
10	1217.5	78.9	297 1	ADT1_DROME
11	1204	78.0	301 1	ADT1_ANOGA
12	978	63.4	339 1	ADT1_CHLKE
13	778.5	50.5	307 1	ADT3_YEAST
14	772	50.0	308 1	ADT1_CHLRE
15	769	49.8	322 1	ADT1_SCHPO
16	768	49.6	386 1	ADT1_GOSHI
17	766	49.4	313 1	ADT1_NEUCR
18	762.5	49.6	305 1	ADT1_KLUFA
19	760.5	49.3	318 1	ADT2_YEAST
20	750	48.6	387 1	ADT1_MAIZE
21	748	48.5	386 1	ADT1_SOLTU
22	747	48.4	382 1	ADT1_ORYSA
23	744	48.2	387 1	ADT2_MAIZE
24	742.5	48.1	381 1	ADT1_ARATH
25	742.5	48.1	385 1	ADT2_ARATH
26	740	48.0	331 1	ADT1_WHEAT
27	739.5	47.9	386 1	ADT2_SOLTU
28	737.5	47.8	309 1	ADT1_YEAST
29	727	47.1	331 1	ADT2_WHEAT
30	302	19.6	588 1	CMC2_CAEBL
31	300	19.4	330 1	GDC_BOVIN
32	299	19.4	307 1	YO7L_YEAST
33	297	19.2	587 1	CMC3_CAEBL

34	295	19.1	678	1	CMC1_HUMAN	075746	homo sapien
35	289.5	18.8	322	1	GDC_RAT	P16261	rattus norv
36	287.5	18.6	702	1	CMC1_CAEBL	Q21153	caenorhabdi
37	286	18.5	325	1	BMCP_HUMAN	095258	homo sapien
38	285	18.5	332	1	GDC_HUMAN	P16260	homo sapien
39	284	18.4	322	1	BMCP_MOUSE	092252	mus musc
40	282.5	18.3	326	1	YE08_SCHPO	013805	schizosacch
41	280	18.1	675	1	CMC2_HUMAN	Q9ujs0	homo sapien
42	265	17.2	312	1	UCP3_HUMAN	P55916	homo sapien
43	265	17.2	676	1	CMC2_MOUSE	09qxx4	mus musc
44	265	17.2	695	1	CMC1_DROME	09va73	drosophila
45	264.5	17.1	309	1	UCP2_PIG	097562	sus scrofa

ALIGNMENTS

RESULT	ID	ADT3_HUMAN	STANDARD:	PRT:	298 AA.
1	ADT3_HUMAN	ADT3_HUMAN	STANDARD:	PRT:	298 AA.
AC	P12236;				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3)				
DE	(ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3).				
GN	SLC25A6 OR ANT3.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
..RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=89236396; PubMed=2541251;				
RA	Cozens A.L., Runswick M.J., Walker J.E.;				
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial				
RT	ADP/ATP translocase.";				
RL	J. Mol. Biol. 206:261-280(1989).				
..RN	[2]				
RP	SEQUENCE OF 36-298 FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=88124845; PubMed=2829183;				
RA	Houldsworth J., Altardi G.;				
RT	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA				
RT	level in adult human liver.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).				
..CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE				
..CC	MITOCHONDRIAL INNER MEMBRANE.				
..CC	-1- SUBUNIT: HOMODIMER.				
..CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL				
..CC	INNER MEMBRANE.				
..CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.				
..CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.				
..CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
..CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -				
..CC	the European Bioinformatics Institute. There are no restrictions on its				
..CC	use by non-profit institutions as long as its content is in no way				
..CC	modified and this statement is not removed. Usage by and for commercial				
..CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
..CC	or send an email to license@isb-sib.ch).				
..CC	-----				
DR	EMBL: J03592; AAA36750.1; -				
DR	PIR: S03894; S03894.				
DR	PIR: B28116; B28116.				
DR	MIM: 300151; -				
DR	MIM: 403000; -				
DR	InterPro: IPR001993; -				
DR	InterPro: IPR002067; -				
DR	InterPro: IPR002113; -				
DR	Pfam: PF00153; mito.carr.1.				
DR	PRINTS: PR00926; MITOCARRIER.				
DR	PRINTS: PR00927; ADPTNSLASE.				

RT "The human fibroblast adenine nucleotide translocator gene. Molecular cloning and sequence.";
 RL J. Biol. Chem. 265:16060-16063(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87166056; PubMed=3031073;
 RA Battisti R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
 Baserga R.;
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated";
 RL J. Biol. Chem. 262:4355-4358(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraia R.,
 Mazzarella R.A., Schlessinger D., Chen E.Y.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Becker M., Graves T., Ozersky P.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 47-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Altardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC -----
 DR EMBL: M57424; AAA51737.1; -;
 DR EMBL: J02683; AAA35579.1; -;
 DR EMBL: L78810; AAB39266.1; -;
 DR EMBL: AC004000; AAB96347.1; -;
 DR EMBL: J03591; AAA36749.1; -;
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR MIM: 300150; -;
 DR InterPro: IPR001993; -;
 DR InterPro: IPR002067; -;
 DR InterPro: IPR002113; -;
 DR Pfam: PF00153; mito_carr.1.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLASE.
 DR PROSITE: PS00215; MITOCH_CARRIER.3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).

FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;
 Query Match 94.8%, Score 1463; DB 1; Length 298;
 Best Local Similarity 92.9%; Pred. No. 5,4e-123;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
 OY 1 MTEQATSFRAKPEFLAGGIAATSKTAVPIERKLLLOVQHASKOIAAKOKYGVDCIVR 60
 DB 1 MTDAAVSFAKDFLAGVAAAIKSTAVPIERKLLLOVQHASKOITADOKYGIIDCVVR 60
 OY 61 IPKEGVLSFPMGNLANIYRFPFQALNFAFKDKYKQIFLGVGDHKTQPMFPAAGNLASG 120
 DB 61 IPKEGVLSFPMGNLANIYRFPFQALNFAFKDKYKQIFLGVGDHKTQPMFPAAGNLASG 120
 OY 121 GAAGATSLCFYVPLDFATRLAADVKGSGTEREPGLDCLVKITKSGICGLYOGFSVS 180
 DB 121 GAAGATSLCFYVPLDFATRLAADVKGSGTEREPGLDCLVKITKSGICGLYOGFSVS 180
 OY 181 VGGIITVRAAYGVYDTAKGMLPDPKNTIYVSMIAQTVAVAGVSPPTVRRMM 240
 DB 181 VGGIITVRAAYGVYDTAKGMLPDPKNTIYVSMIAQTVAVAGVSPPTVRRMM 240
 OY 241 QSGRKADIMYTGTVDCWRKIFRDEGKAFKGAWSNVLKMGCAFVLVLDLKK 296
 DB 241 QSGRKADIMYTGTVDCWRKIFRDEGKAFKGAWSNVLKMGCAFVLVLDLKK 296
 RESULT 4
 ADT2_RAT STANDARD; PRT; 298 AA.
 ID ADT2_RAT
 AC 009073;
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ADP/ATP CARRIER PROTEIN, FIBROBLAST ISOCFORM (ADP/ATP TRANSLOCASE 2)
 DE (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC -----
 DR EMBL: D12771; BA02238.1; -;
 DR InterPro: IPR001993; -;
 DR InterPro: IPR002067; -;
 DR InterPro: IPR002113; -;

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DR Pfam: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KM Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EFE35 CRC64;

Query Match          94.0%: Score 1451; DB 1; Length 298;
Best Local Similarity 91.9%: Pred. No. 6.3e-122;
Matches 272; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

OY 1 MTEQASFAKFLAGGIAAISKTAIVAPIERVKLLLOVQHASKOIADKQYGVDCIVR 60
DB 1 MTDAAVSFAKDFLAGGVAALSKTAIVAPIERVKLLLOVQHASKOITADKQYGIIDCVR 60
OY 61 IPKEQGLVSEFWRGNLANVIRYPTQALNFAEKDYKQIFLGVDKHTQFMRYEAGNLASG 120
DB 61 IPKEQGLVSEFWRGNLANVIRYPTQALNFAEKDYKQIFLGVDKHTQFMRYEAGNLASG 120
OY 121 GAAGATSLCEFYPLDFAFTRIAADVGKSGTERERGLDCLVTKSDGIRGLYOGESVS 180
DB 121 GAAGATSLCEFYPLDFAFTRIAADVGKSGTERERGLDCLVTKSDGIRGLYOGESVS 180
OY 181 VQGIITVRAAFYGYDPAKGLPDPKNTHTVSMIAQOTVAVAGVSYEPDVRRRMM 240
DB 181 VQGIITVRAAFYGYDPAKGLPDPKNTHTVSMIAQOTVAVAGVSYEPDVRRRMM 240
OY 241 QSGRKGADIMVTGTVDCWRKIIFDEGKAFKFGAMSVNLKMGAFVLYLYDELK 296
DB 241 QSGRKGADIMVTGTVDCWRKIIFDEGKAFKFGAMSVNLKMGAFVLYLYDELK 296

RESULT 5
ADPT2_MOUSE STANDARD; PRT; 298 AA.
ID ADPT2_MOUSE
AC P51881; 061311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADP, ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
GN SLC25A5 OR ANT2.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA MEDLINE=97059403; PubMed=9903724.
RX Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs.";
RL Mamm. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sheldon J.G.;
RL Thesis (1995), University of Cambridge, U.K.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;

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RA Costet P., Laplace C.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP REVISIONS.
RA Laplace C.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27316; AAC52838.1; -
DR EMBL: U10404; AAA19009.1; -
DR EMBL: X70847; CA50196.1; -
DR MGI: MGI:1353496; SLC25a5.
DR InterPro: IPR001993; -
DR InterPro: IPR002067; -
DR InterPro: IPR002113; -
DR Pfam: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32931 MW; 0798B04B987EFE20 CRC64;

Query Match          93.6%: Score 1445; DB 1; Length 298;
Best Local Similarity 91.6%: Pred. No. 2.2e-121;
Matches 271; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

OY 1 MTEQASFAKFLAGGIAAISKTAIVAPIERVKLLLOVQHASKOIADKQYGVDCIVR 60
DB 1 MTDAAVSFAKDFLAGGVAALSKTAIVAPIERVKLLLOVQHASKOITADKQYGIIDCVR 60
OY 61 IPKEQGLVSEFWRGNLANVIRYPTQALNFAEKDYKQIFLGVDKHTQFMRYEAGNLASG 120
DB 61 IPKEQGLVSEFWRGNLANVIRYPTQALNFAEKDYKQIFLGVDKHTQFMRYEAGNLASG 120
OY 121 GAAGATSLCEFYPLDFAFTRIAADVGKSGTERERGLDCLVTKSDGIRGLYOGESVS 180
DB 121 GAAGATSLCEFYPLDFAFTRIAADVGKSGTERERGLDCLVTKSDGIRGLYOGESVS 180
OY 181 VQGIITVRAAFYGYDPAKGLPDPKNTHTVSMIAQOTVAVAGVSYEPDVRRRMM 240
DB 181 VQGIITVRAAFYGYDPAKGLPDPKNTHTVSMIAQOTVAVAGVSYEPDVRRRMM 240
OY 241 QSGRKGADIMVTGTVDCWRKIIFDEGKAFKFGAMSVNLKMGAFVLYLYDELK 296
DB 241 QSGRKGADIMVTGTVDCWRKIIFDEGKAFKFGAMSVNLKMGAFVLYLYDELK 296

RESULT 6

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ADT1_RAT
ID ADT1_RAT STANDARD: PRT: 298 AA.
AC Q05962:
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
DE TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
GN SLIC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY, AND WISTAR: TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinohara Y., Kanida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochem. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
CC EXTENT, IN BRAIN AND KIDNEY.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X61667; CAA34842.1; -.
DR EMBL: D12770; BAA02337.1; -.
DR InterPro: IPR001993; -.
DR InterPro: IPR002067; -.
DR InterPro: IPR002113; -.
DR Pfam: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6BC320 CRC64;

Query Match 92.3%; Score 1424; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 1.6e-119;
Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

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OY 121 GAGATGTCFVYPLDFARTRLADYKSGTGEREFGRLDCLVTKITKSPGIRKLYOGFSVS 180
DB 121 GAGATGTCFVYPLDFARTRLADYKSGTGEREFGRLDCLVTKITKSPGIRKLYOGFSVS 180
OY 181 VOGIIITPAAFGVYDTAKGMLPDPKNTNHYVSMIAOTVAVAGVSPEDTVRRMM 240
DB 181 VOGIIITPAAFGVYDTAKGMLPDPKNTNHYVSMIAOTVAVAGVSPEDTVRRMM 240
OY 241 OSGRKADIMTGTVDCAKRIKFRDEGKAFKFGASNVLRGMAFVLYVDELKKYI 298
DB 241 OSGRKADIMTGTVDCAKRIKFRDEGKAFKFGASNVLRGMAFVLYVDELKKYI 298

RESULT 7
ADT1_BOVIN
ID ADT1_BOVIN STANDARD: PRT: 297 AA.
AC P02722:
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN, HEART ISOFORM T1 (ADP/ATP TRANSLOCASE 1)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
GN SLIC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
RN [2]
RP SEQUENCE.
RC MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Misra D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RC MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrad H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC -----
DR EMBL: M13783; AAA30363.1; -.
DR EMBL: M24102; AAA30768.1; -.
DR PIR: A03181; XMBO.
DR PIR: A24822; A24822.
DR PIR: A43646; A43646.
DR InterPro: IPR001993; -.
DR InterPro: IPR002067; -.

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DR InterPro: IPR002113; -.
DR Pfam: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KM Mitochondrion; inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Methylation.
FT INIT_MET 0
FT MOD_RES 1 1 BLOCKED.
FT TRANSMEM 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3CA4A0AEB48 CRC64;

Query Match 91.88; Score 1417; DB 1; Length 297;
Best Local Similarity 89.28; Pred. No. 6.6e-119;
Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 2 TEQAISFAKDFLAGIAAISTAVAPIERVKLLQVQHASKOIADKQKGIYDCIYRI 61
   1 SDQALSFKDFLAGVAIAIKSTANAPIERVKLLQVQHASKOISAEKQGIIDCVRI 60
DB 1 PKEGGLSFWRGNLANVIRYPTQALNFARFKDKYKQIFLGVDKHTQFWRRFAGMLASGG 120
QY 62 PKEGGLSFWRGNLANVIRYPTQALNFARFKDKYKQIFLGVDKHTQFWRRFAGMLASGG 121
   1 PKEGGLSFWRGNLANVIRYPTQALNFARFKDKYKQIFLGVDKHTQFWRRFAGMLASGG 120
DB 61 PKEGGLSFWRGNLANVIRYPTQALNFARFKDKYKQIFLGVDKHTQFWRRFAGMLASGG 120
QY 122 AAGATSLCFEYPLDFAFRLADVGKSGTEREFGSLGDCLVKTFKSDGIRGLYQGFSSVS 181
   121 AAGATSLCFEYPLDFAFRLADVGKGAQREFTGLGNCITKIFKSDGIRGLYQGFSSVS 180
DB 182 QGIIITRAAYEGYVDATKAGMLPDPKNTIIVSWMIQTVTAAGVSYPTDVRRRMM 241
   181 QGIIITRAAYEGYVDATKAGMLPDPKNTIIVSWMIQTVTAAGVSYPTDVRRRMM 240
QY 242 SGRGADIMYTGTVDCMRKIFRDEGKAFKFGAMSNVLRMGGAFLVLYDELKVI 298
   241 SGRGADIMYTGTVDCMRKIFRDEGKAFKFGAMSNVLRMGGAFLVLYDEIKKFV 297
DB 241 SGRGADIMYTGTVDCMRKIFRDEGKAFKFGAMSNVLRMGGAFLVLYDEIKKFV 297

RESULT 8
ADT1_MOUSE
ID ADT1_MOUSE STANDARD; PRT; 298 AA.
AC P48962;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADP, ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
DE TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLATOR 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RG STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs."
RL Mamm. Genome 7:25-30(1996).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL

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CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC -----
DR EMBL: U27315; AAC52837.1; -.
DR MGD: MGI:1353495; SLC25a4.
DR InterPro: IPR001993; -.
DR InterPro: IPR002067; -.
DR InterPro: IPR002113; -.
DR Pfam: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KM Mitochondrion; inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32870 MW; 3ZAC3BAEFC4F482 CRC64;

Query Match 91.58; Score 1412; DB 1; Length 298;
Best Local Similarity 88.68; Pred. No. 1.9e-118;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVQHASKOIADKQKGIYDCIYRI 60
   1 MGDQALSFKDFLAGIAAISTAVAPIERVKLLQVQHASKOISAEKQGIIDCVRI 60
DB 1 MGDQALSFKDFLAGIAAISTAVAPIERVKLLQVQHASKOISAEKQGIIDCVRI 60
QY 61 IPKEGGLSFWRGNLANVIRYPTQALNFARFKDKYKQIFLGVDKHTQFWRRFAGMLASG 120
   1 IPKEGGLSFWRGNLANVIRYPTQALNFARFKDKYKQIFLGVDKHTQFWRRFAGMLASG 120
DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFARFKDKYKQIFLGVDKHTQFWRRFAGMLASG 120
QY 121 GAAGATSLCFEYPLDFAFRLADVGKSGTEREFGSLGDCLVKTFKSDGIRGLYQGFSSVS 180
   121 GAAGATSLCFEYPLDFAFRLADVGKSSOREFNGSLGDCITKIFKSDGIRGLYQGFSSVS 180
DB 121 GAAGATSLCFEYPLDFAFRLADVGKSSOREFNGSLGDCITKIFKSDGIRGLYQGFSSVS 180
QY 181 VOGIIITRAAYEGYVDATKAGMLPDPKNTIIVSWMIQTVTAAGVSYPTDVRRRMM 240
   181 VOGIIITRAAYEGYVDATKAGMLPDPKNTIIVSWMIQTVTAAGVSYPTDVRRRMM 240
DB 181 VOGIIITRAAYEGYVDATKAGMLPDPKNTIIVSWMIQTVTAAGVSYPTDVRRRMM 240
QY 241 QSGRKGADIMYTGTVDCMRKIFRDEGKAFKFGAMSNVLRMGGAFLVLYDELKVI 298
   241 QSGRKGADIMYTGTVDCMRKIFRDEGKAFKFGAMSNVLRMGGAFLVLYDEIKKFV 298
DB 241 QSGRKGADIMYTGTVDCMRKIFRDEGKAFKFGAMSNVLRMGGAFLVLYDEIKKFV 298

RESULT 9
ADT1_HUMAN
ID ADT1_HUMAN STANDARD; PRT; 298 AA.
AC P12235;
DT 01-NOV-1990 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADP, ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
DE TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLATOR 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

```

OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=89340499; PubMed=2547778;
 RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
 RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
 RT "A human muscle adenine nucleotide translocator gene has four exons,
 RT is located on chromosome 4, and is differentially expressed.";
 RL J. Biol. Chem. 264:13998-14004(1989).
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=88041149; PubMed=2823266;
 RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
 RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
 RT of a leader peptide, divergence from a fibroblast translocator cDNA,
 RT and coevolution with mitochondrial DNA genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
 RN [4]
 RN SEQUENCE OF 1-37 FROM N.A.
 RC Tissue-Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC -----
 DR EMBL: J02966; AAA61223.1; -;
 DR EMBL: J03593; AAA36751.1; -;
 DR EMBL: J04982; AAA51736.1; -;
 DR PIR: A28116; A28116;
 DR PIR: A39891; A39891;
 DR PIR: S03893; S03893;
 DR PIR: A44778; A44778;
 DR MIM: 103220; -;
 DR InterPro: IPR001993; -;
 DR InterPro: IPR002067; -;
 DR InterPro: IPR002113; -;
 DR Pfam: PF00153; mito_carr; 1;
 DR PRINTS: PRO0926; MITOCARRIER;
 DR PRINTS: PRO0927; ADPTRNSLCASE;
 DR PROSITE: PS00215; MITOCH_CARRIER; 3;
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family;
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.

FT REPEAT 209 298 3.
 FT CONFLICT 16 16 G -> A (IN REF. 3).
 FT CONFLICT 147 149 GGA -> RR (IN REF. 3).
 FT CONFLICT 227 227 V -> L (IN REF. 3).
 SO SEQUENCE 298 AA; 33064 MW; 59F0DFAE04EFCFB6; CRC64;
 Query Match 91.3%; Score 1409; DB 1; Length 298;
 Best Local Similarity 88.3%; Pred. No. 3,4e-118;
 Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;
 OY 1 MTEDAISFAKPLFLAGIAAISKRAVAPIERVKLLLOVHASKQIADKQYKGYDCTVR 60
 DB 1 MGDHAMSFLKPLFLAGVAAVSKTAVAPIERVKLLLOVHASKQISAEKQYKGYDCTVR 60
 OY 61 IPKRGVLSFWRGNLANVIRFPPQALNFAFKDKYKQIFLGVDKHNQFMFYPAGNLASG 120
 DB 61 IPKRGVLSFWRGNLANVIRFPPQALNFAFKDKYKQIFLGVDKHNQFMFYPAGNLASG 120
 OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGGLDCLVKITKSDINGLYOGFSVS 180
 DB 121 GAAGATSLCFYVPLDFARTRLAADVGKGAQREFHGLGDCIIKIFKSDGLRGLYOGFVVS 180
 OY 181 VGGITTRAAVFGYDTAKGMLPDKNTHIVYVSMIAQTVTAAGVVSYPEDTVRRRMM 240
 DB 181 VGGITTRAAVFGYDTAKGMLPDKNTHIVYVSMIAQTVTAAGVVSYPEDTVRRRMM 240
 OY 241 QSGRKGADIMYTGIVDCKRIIFRDEGKAPFKGAMSNVLRGAGFVLYLDELKVI 298
 DB 241 QSGRKGADIMYTGIVDCKRIIFRDEGKAPFKGAMSNVLRGAGFVLYLDELKVI 298
 RESULT 10
 ADT_DROME STANDARD; PRT: 297 AA.
 ID ADT_DROME STANDARD; PRT: 297 AA.
 AC Q26365; Q26254; P91614; Q9VZ70;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ADP-ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
 DE TRANSLOCATOR) (ANT) (STRESS SENSITIVE B PROTEIN).
 GN SEB OR A/A-T OR CG16944.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92389367; PubMed=1387687;
 RA Louvi A., Tsitlilou S.G.;
 RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
 RT melanogaster shows a high degree of similarity with the mammalian
 RT ADP/ATP translocases.";
 RL J. Mol. Evol. 35:44-50(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=94350065; PubMed=7520869;
 RA Hutter P., Karch F.;
 RT "Molecular analysis of a candidate gene for the reproductive
 RT isolation between sibling species of Drosophila.";
 RL Experientia 50:749-762(1994).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN-OREGON-R;
 RA Zhang Y.Q., Davis A.W., Roote J., Hermann S., Ashburner M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

DR InterPro: IPR002067; -
 DR InterPro: IPR002113; -
 DR Pfam: PF00153; mito_carr; 1.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER, 3.
 DR MitoChondrion; Inner membrane; Repeat; Transmembrane; Transport.
 KW TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 216 233 5 (POTENTIAL).
 FT TRANSMEM 275 293 6 (POTENTIAL).
 SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;

Query Match 78.08; Score 1204; DB 1; Length 301;
 Best Local Similarity 77.78; Pred. No. 6e-100;
 Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

QY 1 MTEGAD--ISFAKDFLAGGIAAISTAVAPIERVKLLQVHASKQIADKQYKGIYDCI 58
 Db 1 MTKKADPYGFAKDFLAGGISAANSKTAVAPIERVKLLQVHASKQIADKQYKGIYDCI 60
 QY 59 VRIPEGVLSFWRGNLAVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLA 118
 Db 61 VRIPEGVLSFWRGNLAVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLA 120
 QY 119 SGGAGATSLCFVYPLDFARTRLADVGKSTEREFRGLDCLVTKTSQDGRGLYQGS 178
 Db 121 SGGAGATSLCFVYPLDFARTRLADVGKSTEREFRGLDCLVTKTSQDGRGLYQGS 180
 QY 179 VSVGGIITIRAYRGVVDATAGMLPDPKNTIIVSMMIAQVTAVAGVSVFPTVRRRM 238
 Db 181 VSVGGIITIRAYRGVVDATAGMLPDPKNTIIVSMMIAQVTAVAGVSVFPTVRRRM 240
 QY 239 MMSGKRGADIMYTVDCWKRIFRDEGKAFFKGAWSNVLRGMAFVLVYDELKVI 298
 Db 241 MMSGKRGADIMYTVDCWKRIFRDEGKAFFKGAWSNVLRGMAFVLVYDELKVI 300

RESULT 12
 ADT_CHLKE STANDARD; PRT; 339 AA.
 AC P31692;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADP/ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
 DE TRANSLOCATOR) (ANT).
 OS Chlorella keesleri.
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorella.
 OX NCBI_TaxID=3074;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92084708; PubMed=1748677;
 RA Hilgarch C., Sauer N., Tanner W.;
 RT "Glucose increases the expression of the ATP/ADP translocator and the
 RT glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";
 RL J. Biol. Chem. 266:24044-24047(1991).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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DR EMBL: M76669; AAA33027.1; -
 DR PTR: A41677; A41677.
 DR InterPro: IPR001993; -
 DR InterPro: IPR002067; -
 DR InterPro: IPR002113; -
 DR Pfam: PF00153; mito_carr; 1.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER, 3.
 DR MitoChondrion; Inner membrane; Repeat; Transmembrane; Transport.
 KW TRANSMEM 45 62 1 (POTENTIAL).
 FT TRANSMEM 108 126 2 (POTENTIAL).
 FT TRANSMEM 151 168 3 (POTENTIAL).
 FT TRANSMEM 209 228 4 (POTENTIAL).
 FT TRANSMEM 248 265 5 (POTENTIAL).
 FT TRANSMEM 304 322 6 (POTENTIAL).
 SQ SEQUENCE 339 AA; 36686 MW; 54779734A33B3942 CRC64;

Query Match 63.48; Score 978; DB 1; Length 339;
 Best Local Similarity 66.98; Pred. No. 8.6e-80;
 Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

QY 6 ISFAKDFLAGGIAAISTAVAPIERVKLLQVHASKQIADK--QYKIVDCIVRIPK 63
 Db 39 MAFVKDLAAGTAGAISTAVAPIERVKLLQVHASKQIADK--QYKIVDCIVRIPK 98
 QY 64 EGVLSFWRGNLAVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLAAGAA 123
 Db 99 EGVLSFWRGNLAVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLAAGAA 157
 QY 124 GATSLCFVYPLDFARTRLADVGKSTEREFRGLDCLVTKTSQDGRGLYQGSVYQ 183
 Db 158 GATSLCFVYPLDFARTRLADVG--SGKSRFTGLVDCISKYVKKGGPMALVQGGVSVQ 216
 QY 184 IIVIRAYFGVYDPAKAGMLPDPKNTIIVSMMIAQVTAVAGVSVFPTVRRRMMS 242
 Db 217 IIVIRAYFGVYDPAKAGMLPDPKNTIIVSMMIAQVTAVAGVSVFPTVRRRMMS 276
 QY 243 GRKGADIMYTVDCWKRIFRDEGKAFFKGAWSNVLRGMAFVLVYDELKVI 298
 Db 277 --GGERQYNGTIDCMKRVAAQOEGKMAFFKGAWSNVLRGMAFVLVYDELKVI 329

RESULT 13
 ADT3_YEAST STANDARD; PRT; 307 AA.
 AC P18238;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE ADP/ATP CARRIER PROTEIN 3 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE
 DE TRANSLOCATOR 3) (ANT 3).
 GN AAC3 OR YBR085W OR YBR0753.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90324269; PubMed=2165073;
 RA Kolarov J., Kolarova N., Nelson N.;
 RT "A third ADP/ATP translocator gene in yeast.";
 RL J. Biol. Chem. 265:12711-12716(1990).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=5288C;
 CC Andre B., Cziepluch C., Hein C., Jauniaux J.C., Urrestarazu A.,
 CC Vissers S.;
 CC Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.

Db 239 RRMWTS---GSAYKYNSSFFHCEIIVKNECMKSLFKGAGANILRAVAGAGVAGYDOLQ 295
 QY 296 KVI 298
 Db 296 VIL 298

RESULT 15

ADT_SCHPO STANDARD; PRT; 322 AA.

AC 001988; ID ADT_SCHPO
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE ADP_CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT)
 GN ANCI OR SPBC530.10C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=96257204; PubMed=8675018;
 RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae."
 RL Gene 171:113-117(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=96257204; PubMed=8675018;
 RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae."
 RL Gene 171:113-117(1996).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC
 DR EMBL; Z49974; CA90275.1; -
 DR EMBL; AL023634; CAA19176.1; -
 DR HSP; P04002; IATF.
 DR InterPro: IPR001993; -
 DR InterPro: IPR002067; -
 DR InterPro: IPR002113; -
 DR Pfam; PF00153; mito_carr; 1.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00927; ADPTRNSLCASE.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 28 48 1 (POTENTIAL).
 FT TRANSMEM 93 111 2 (POTENTIAL).
 FT TRANSMEM 131 151 3 (POTENTIAL).
 FT TRANSMEM 197 217 4 (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT TRANSMEM 289 309 6 (POTENTIAL).
 SO SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;

Query Match 49.8%; Score 769; DB 1; Length 322;
 Best Local Similarity 53.6%; Pred. No. 3,2e-61;
 Matches 158; Conservative 50; Mismatches 75; Indels 12; Gaps 6;
 QY 7 SPADFLLAGIAAIAISKRAVAPIERVKLLLOVHAKNOIADK---QYKGVDCIVRIPK 63
 Db 26 TFFDFEMMGVSAVSKTAAPIERVKLLIQNQ--DEMIRAGRISHRYKGIGECFKRTAA 83
 QY 64 EGVLSFWRGNLANVIRYFPQALNFAFKDKYKQIFLGVNKHQFWRYPAGNLASGAA 123
 Db 84 EGVLSLWRGNLANVIRYFPQALNFAFKDKYKMF--CYKNERDGYAKMFWGNLASGAA 142
 QY 124 GATSLCEVYPLDFAFRTLAADV--GKSGTEREPFGLDCLVYKTSQIGRLYGQFSVS 181
 Db 143 GAASLLEFVSLDVARTRLANDAKSAKKGQERQFNGLVYVRYKTYRSDGLRGLRGFGPSV 202
 QY 182 QGIIIRAAVYGVVDLAG--MLPDPKNTIYVSMKIAQTVAAVGVVSPPDYVRRRMM 240
 Db 203 VGIIVYRGLYRGMYDTLPVLPVLPLEGNPLASFLGLGVAVTGSGVASYPLDTIRRRMM 262
 QY 241 QSGRKADIMYTGIVDCWRKIFRDEGKAFKFGAMSNVLRGMGAFVLYDELK 295
 Db 263 TSGEA---VKYSSFEQGRQILAKEGARSPFKGAGANILRGVAGAGVSTYDQV 314

Search completed: April 29, 2001, 11:39:14
 Job time: 128 sec

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OM protein - protein search, using sw model

Run on: April 29, 2001, 11:35:45 ; Search time 16.58 seconds
(without alignments)
1235.189 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543
Sequence: 1 MTEQAIISFAKDFLAGGIAA.....LRMGGAFLVLYDELKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	1 S03894	ADP,ATP carrier pr
2	1512	98.0	298	1 B43646	ADP,ATP carrier pr
3	1454	94.2	298	1 A29132	ADP,ATP carrier pr
4	1424	92.3	298	1 T60173	adenine nucleotide
5	1422	92.2	298	1 XWBO	ADP,ATP carrier pr
6	1418	91.9	298	1 S37210	ADP,ATP carrier pr
7	1409	91.3	298	1 A44778	ADP,ATP carrier pr
8	1405	91.1	298	1 S31814	ADP,ATP carrier pr
9	1184	76.7	301	1 S31935	ADP,ATP carrier pr
10	1041	67.5	313	1 T23207	hypothetical prote
11	1039	67.3	313	1 T25850	hypothetical prote
12	1038	67.3	300	1 T25371	hypothetical prote
13	993.5	64.4	300	1 T15206	hypothetical prote
14	978	63.4	339	2 A41677	ADP,ATP carrier pr
15	943	61.1	301	2 S51132	ADP,ATP carrier pr
16	778.5	50.5	307	2 A36582	ADP,ATP carrier pr
17	772	50.0	308	1 S30259	ADP,ATP carrier pr
18	769	49.8	322	2 T40526	ADP,ATP translocas
19	768	49.8	386	2 T09709	ADP,ATP carrier pr
20	766	49.6	313	1 XWNC	ADP,ATP carrier pr
21	764	49.5	326	2 T25728	hypothetical prote
22	762.5	49.4	305	2 S68154	ADP,ATP carrier pr
23	760.5	49.3	318	1 A31978	ADP,ATP carrier pr
24	756.5	49.0	306	2 T20012	hypothetical prote
25	750	48.6	387	2 S14876	ADP,ATP carrier pr
26	748	48.5	386	2 S21974	ADP,ATP carrier pr
27	747	48.4	306	2 T42011	ADP,ATP carrier pr
28	747	48.4	386	2 S17917	ADP,ATP carrier pr
29	744	48.2	387	2 S16568	ADP,ATP carrier pr

30	743	48.2	379	2 T04608	ADP,ATP carrier pr
31	742.5	48.1	385	1 S29852	ADP,ATP carrier pr
32	742	48.1	382	2 S33630	ADP,ATP carrier pr
33	739.5	47.9	386	2 S14874	ADP,ATP carrier pr
34	737.5	47.8	309	2 A24849	ADP,ATP carrier pr
35	734.5	47.6	379	2 S21313	ADP,ATP carrier pr
36	681.5	44.2	298	2 T24029	hypothetical prote
37	520.5	33.7	327	2 T51577	ADP,ATP translocas
38	383	24.8	325	2 T04273	hypothetical prote
39	381	24.7	352	2 T01729	mitochondrial solu
40	372	24.1	358	2 T45934	hypothetical prote
41	370.5	24.0	415	2 T48171	hypothetical prote
42	369.5	23.9	381	2 T51158	hypothetical prote
43	368	23.8	475	2 T50686	peroxisomal Ca-dep
44	344.5	22.3	332	2 T47703	Ca-dependent solut
45	321.5	20.8	479	2 T49871	peroxisomal Ca-dep

ALIGNMENTS

RESULT 1
S03894
ADP,ATP carrier protein T3 - human
N:Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP,
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
R:Accession: S03894; B28116
R:Cozens, A.L., Runswick, M.J., Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; MUID:89236396
A:Accession: S03894
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; MUID:88124845
A:Accession: B28116
A:Molecule type: mRNA
A:Residues: 36-104, 'R', 106, 'A', 109-298 <HO>
A:CROSS-references: GB:J03592; NID:9339722; PIDN:AAA36750.1; PID:9339723
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT3; ANT3Y
A:CROSS-references: GDB:125184; OMIM:300151; OMIM:403000
A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP,ATP carrier protein #status predicted <ANT>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1543; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 6.4e-129;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	MTEQAIISFAKDFLAGGIAAISKTAIVAPRIERVKLLQVQHASKOIAADKQKGIYDCIVR	60
Db	1	MTEQAIISFAKDFLAGGIAAISKTAIVAPRIERVKLLQVQHASKOIAADKQKGIYDCIVR	60
Oy	61	IPKEGVLSFMRGNLANVIRFPYQALNFAFKDKYKQIFLCGVDKHTQFMRYFAGNLASG	120
Db	61	IPKEGVLSFMRGNLANVIRFPYQALNFAFKDKYKQIFLCGVDKHTQFMRYFAGNLASG	120
Oy	121	GAAGTSLCFYVPLDFATRLAADVGKSGTEREPFGADCDLVKTKSGSIGLVQGFSSVS	180
Db	121	GAAGTSLCFYVPLDFATRLAADVGKSGTEREPFGADCDLVKTKSGSIGLVQGFSSVS	180
Oy	121	GAAGTSLCFYVPLDFATRLAADVGKSGTEREPFGADCDLVKTKSGSIGLVQGFSSVS	180
Db	121	GAAGTSLCFYVPLDFATRLAADVGKSGTEREPFGADCDLVKTKSGSIGLVQGFSSVS	180

QY 181 VGGIIIRAAAFGVYDFAKGMILPDPKNTHTIVSMIAQTVTAAGVVSYPEDTVRRMM 240
 |||||||
 Db 181 VGGIIIRAAAFGVYDFAKGMILPDPKNTHTIVSMIAQTVTAAGVVSYPEDTVRRMM 240
 |||||||

QY 241 QSGRRGADIMYTGIVDCWRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 298
 |||||||
 Db 241 QSGRRGADIMYTGIVDCWRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 298
 |||||||

RESULT 2

B43646
 ADP/ATP carrier protein T2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differentially in
 A:Reference number: A43646; MUID:89229093
 A:Accession: B43646
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match Best Local Similarity 98.0%; Score 1512; DB 2; Length 298;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHASKOIAADKOYKGIIVDCIVR 60
 |||||||
 Db 1 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHASKOIAADKOYKGIIVDCIVR 60
 |||||||

QY 61 IPKQGVLSFWRGNLANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAAG 120
 |||||||
 Db 61 IPKQGVLSFWRGNLANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAAG 120
 |||||||

QY 121 GAAGATSLCFYPPIDFATRIAAADVGSKGTERRERGLDCLVTKTSKGIRGLVQGFSSV 180
 |||||||
 Db 121 GAAGATSLCFYPPIDFATRIAAADVGSKGTERRERGLDCLVTKTSKGIRGLVQGFSSV 180
 |||||||

QY 181 VGGIIIRAAAFGVYDFAKGMILPDPKNTHTIVSMIAQTVTAAGVVSYPEDTVRRMM 240
 |||||||
 Db 181 VGGIIIRAAAFGVYDFAKGMILPDPKNTHTIVSMIAQTVTAAGVVSYPEDTVRRMM 240
 |||||||

QY 241 QSGRRGADIMYTGIVDCWRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 298
 |||||||
 Db 241 QSGRRGADIMYTGIVDCWRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 298
 |||||||

RESULT 3

A29132
 ADP/ATP carrier protein T2 - human
 A:Alternate names: mitochondrial ADP/ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132; C28116
 R:Batlini, R.; Ferrali, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 267, 4355-4359, 1992
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat
 A:Reference number: A29132; MUID:87160056
 A:Accession: A29132
 A:Molecule type: mRNA
 A:Residues: 1-298 <BAT>
 A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
 R:Houldsworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'G', 67-110, 'U', 112-161, 'G', 163-298 <HOU>
 A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
 A:Experimental source: clone PHAT3
 C:Genetics:

A:Gene: ANT2; T3; 2F1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-Xq26
 A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match Best Local Similarity 94.2%; Score 1454; DB 1; Length 298;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHASKOIAADKOYKGIIVDCIVR 60
 |||||||
 Db 1 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHASKOIAADKOYKGIIVDCIVR 60
 |||||||

QY 61 IPKQGVLSFWRGNLANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAAG 120
 |||||||
 Db 61 IPKQGVLSFWRGNLANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAAG 120
 |||||||

QY 121 GAAGATSLCFYPPIDFATRIAAADVGSKGTERRERGLDCLVTKTSKGIRGLVQGFSSV 180
 |||||||
 Db 121 GAAGATSLCFYPPIDFATRIAAADVGSKGTERRERGLDCLVTKTSKGIRGLVQGFSSV 180
 |||||||

QY 181 VGGIIIRAAAFGVYDFAKGMILPDPKNTHTIVSMIAQTVTAAGVVSYPEDTVRRMM 240
 |||||||
 Db 181 VGGIIIRAAAFGVYDFAKGMILPDPKNTHTIVSMIAQTVTAAGVVSYPEDTVRRMM 240
 |||||||

QY 241 QSGRRGADIMYTGIVDCWRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 296
 |||||||
 Db 241 QSGRRGADIMYTGIVDCWRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 296
 |||||||

RESULT 4

I60173
 adenine nucleotide translocator - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 C:Accession: I60173
 R:Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
 Biochim. Biophys. Acta 1152, 192-196, 1993
 A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding r
 A:Reference number: I60173; MUID:94002161
 A:Accession: I60173
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-298 <RES>
 A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
 C:Genetics:
 A:Gene: ant1
 C:Introns: 37/3; 200/1; 247/1
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match Best Local Similarity 92.3%; Score 1424; DB 2; Length 298;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

OY 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTLVSMIAQTAVAGVSYSPDVTVRMM 240
 Db 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTLVSMIAQTAVAGVSYSPDVTVRMM 240
 OY 241 QSGRKGADIMYTGVDWCRRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKYY 298
 Db 241 QSGRKGADIMYTGVDWCRRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKYY 298

RESULT 7

A44778

ADP/ATP carrier protein T1 - human

N:Alternate names: mitochondrial ADP/ATP translocase 1

C:Species: Homo sapiens (man)

C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: A44778; S03893; A39891; A28116

R:Lit., K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.

J. Biol. Chem. 264, 13998-14004, 1989

A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located

A:Reference number: A44778; MUID:89340499

A:Accession: A44778

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-298 <LTA>

A:Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659

R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.

J. Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr

A:Reference number: S03893; MUID:99236396

A:Accession: S03893

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 <COZ>

R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.

Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987

A:Title: CDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader

A:Reference number: A39891; MUID:88041149

A:Accession: A39891

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>

A:Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920

R:Experimental source: clone pMAN7

R:Houldsworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A94197; MUID:88124845

A:Accession: A28116

A:Molecule type: mRNA

A:Residues: 1-37 <HOU>

A:Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1; PID:g339725

A:Experimental source: liver

C:Genetics:

A:Gene: GDB:ANT1; T1

A:Cross-references: GDB:119680; OMIM:103220

A:Map position: 4q35-4q35

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 91.3%; Score 1409; DB 1; Length 298;

Best Local Similarity 88.3%; Pred. No. 4.5e-117;

Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

OY 1 MTEQAIISFADFLAGIAAISKTAIVAPIERVKLLLOVHASKIOIADKQYKGIIVDCIVR 60
 Db 1 MGDHANSFLDFLAGIAAISKTAIVAPIERVKLLLOVHASKIOIADKQYKGIIVDCIVR 60
 OY 61 IPKQGVLSFWKGNLANVIRYFPQALNFAFKDKYKQIFLGGVDKHTQFWRYPAGNLASG 120

Db 61 IPKQGVLSFWKGNLANVIRYFPQALNFAFKDKYKQIFLGGVDKHTQFWRYPAGNLASG 120
 OY 121 GAAGATSLCFYPLDFAFTRILAAVNGSGTFRERGLDGLVTKTKSDGIRGLYOGFSVS 180
 Db 121 GAAGATSLCFYPLDFAFTRILAAVNGSGTFRERGLDGLVTKTKSDGIRGLYOGFSVS 180
 OY 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTLVSMIAQTAVAGVSYSPDVTVRMM 240
 Db 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTLVSMIAQTAVAGVSYSPDVTVRMM 240
 OY 241 QSGRKGADIMYTGVDWCRRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKYY 298
 Db 241 QSGRKGADIMYTGVDWCRRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKYY 298

RESULT 8

S31814

ADP/ATP carrier protein T2 - mouse

N:Alternate names: adenine nucleotide translocase

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998

C:Accession: S31814

R:Costet, P.; Laplace, C.

submitted to the EMBL Data Library, January 1993

A:Reference number: S31814

A:Accession: S31814

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <COS>

A:Cross-references: EMBL:X70847

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 91.1%; Score 1405; DB 2; Length 298;

Best Local Similarity 89.2%; Pred. No. 1e-116;

Matches 264; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

OY 1 MTEQAIISFADFLAGIAAISKTAIVAPIERVKLLLOVHASKIOIADKQYKGIIVDCIVR 60
 Db 1 MTEQAIISFADFLAGIAAISKTAIVAPIERVKLLLOVHASKIOIADKQYKGIIVDCIVR 60
 OY 61 IPKQGVLSFWKGNLANVIRYFPQALNFAFKDKYKQIFLGGVDKHTQFWRYPAGNLASG 120
 Db 61 IPKQGVLSFWKGNLANVIRYFPQALNFAFKDKYKQIFLGGVDKHTQFWRYPAGNLASG 120
 OY 121 GAAGATSLCFYPLDFAFTRILAAVNGSGTFRERGLDGLVTKTKSDGIRGLYOGFSVS 180
 Db 121 GAAGATSLCFYPLDFAFTRILAAVNGSGTFRERGLDGLVTKTKSDGIRGLYOGFSVS 180
 OY 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTLVSMIAQTAVAGVSYSPDVTVRMM 240
 Db 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTLVSMIAQTAVAGVSYSPDVTVRMM 240
 OY 241 QSGRKGADIMYTGVDWCRRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKYY 296
 Db 241 QSGRKGADIMYTGVDWCRRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKYY 296

RESULT 9
 S31935
 ADP/ATP carrier protein - African malaria mosquito
 C:Species: Anopheles gambiae (African malaria mosquito)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S31935; S31936
 R:Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
 submitted to the EMBL Data Library, February 1993
 A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
 A:Reference number: S31935

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2001, 11:35:20 ; Search time 18.75 Seconds
(Without alignments)
908.514 Million cell updates/sec

Title: US-09-393-441-33
Perfect score: 1543
Sequence: 1 MTEQAISPAKDFLAGGIAA.....LRMGCAFLVLYDEIKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues
Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /SID56/gcgdata/geneseq/AA1980.DAT:*
 - 2: /SID56/gcgdata/geneseq/AA1981.DAT:*
 - 3: /SID56/gcgdata/geneseq/AA1982.DAT:*
 - 4: /SID56/gcgdata/geneseq/AA1983.DAT:*
 - 5: /SID56/gcgdata/geneseq/AA1984.DAT:*
 - 6: /SID56/gcgdata/geneseq/AA1985.DAT:*
 - 7: /SID56/gcgdata/geneseq/AA1986.DAT:*
 - 8: /SID56/gcgdata/geneseq/AA1987.DAT:*
 - 9: /SID56/gcgdata/geneseq/AA1988.DAT:*
 - 10: /SID56/gcgdata/geneseq/AA1989.DAT:*
 - 11: /SID56/gcgdata/geneseq/AA1990.DAT:*
 - 12: /SID56/gcgdata/geneseq/AA1991.DAT:*
 - 13: /SID56/gcgdata/geneseq/AA1992.DAT:*
 - 14: /SID56/gcgdata/geneseq/AA1993.DAT:*
 - 15: /SID56/gcgdata/geneseq/AA1994.DAT:*
 - 16: /SID56/gcgdata/geneseq/AA1995.DAT:*
 - 17: /SID56/gcgdata/geneseq/AA1996.DAT:*
 - 18: /SID56/gcgdata/geneseq/AA1997.DAT:*
 - 19: /SID56/gcgdata/geneseq/AA1998.DAT:*
 - 20: /SID56/gcgdata/geneseq/AA1999.DAT:*
 - 21: /SID56/gcgdata/geneseq/AA2000.DAT:*
 - 22: /SID56/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1 *	1543	100.0	298	21	V71033 Human adenine nucl
2	1454	94.2	298	21	V71032 Human adenine nucl
3	1412	91.5	298	19	W61169 Anti protein. Mus
4	1385.5	89.8	297	21	V71031 Human adenine nucl
5	742.5	48.1	346	21	G36577 Arabidopsis thalia
6	742.5	48.1	346	21	G37261 Arabidopsis thalia
7	742.5	48.1	346	21	G37264 Arabidopsis thalia
8	742.5	48.1	346	21	G38460 Arabidopsis thalia
9	742.5	48.1	363	21	G37260 Arabidopsis thalia
10	742.5	48.1	363	21	G37260 Arabidopsis thalia
11	742.5	48.1	363	21	G37263 Arabidopsis thalia

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB ID	Description
1	V71033	1543	100.0	298	21	V71033 Human adenine nucl
2	V71032	1454	94.2	298	21	V71032 Human adenine nucl
3	W61169	1412	91.5	298	19	W61169 Anti protein. Mus
4	V71031	1385.5	89.8	297	21	V71031 Human adenine nucl
5	G36577	742.5	48.1	346	21	G36577 Arabidopsis thalia
6	G37261	742.5	48.1	346	21	G37261 Arabidopsis thalia
7	G37264	742.5	48.1	346	21	G37264 Arabidopsis thalia
8	G38460	742.5	48.1	346	21	G38460 Arabidopsis thalia
9	G37260	742.5	48.1	363	21	G37260 Arabidopsis thalia
10	G37260	742.5	48.1	363	21	G37260 Arabidopsis thalia
11	G37263	742.5	48.1	363	21	G37263 Arabidopsis thalia

29-AUG-2000 (first entry)

Human adenine nucleotide translocator ANF3.

Human: adenine nucleotide translocator; ANF3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nocotropic; antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; antiproliferative; cerebroprotective; therapeutic; screening; postnatal; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.

Homo sapiens.

MO200026370-A2.

11-MAY-2000.

03-NOV-1999; 99WO-US25883.

03-NOV-1998; 98US-0185904.

08-SEP-1999; 99US-0393441.

(MITO-) MITOKOR.

Pt Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
Pi Ghosh SS;
XX
DR WPI: 2000-365619/31.
DR N-PDSB: D00521.
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease
XX
PS Claim 46; Page 173-174; 175pp; English.
XX
CC The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC d(ATP)-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MENAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT3 from human brain.

Sequence 298 AA;

KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 XX
 OS Homo sapiens.
 XX
 PN W0200026370-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 03-NOV-1999; 99WO-US5883.
 XX
 PR 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0339441.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX
 XX WPI: 2000-365619/31.
 DR N-PSDB: D00520.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e. g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 XX Claim 45; Page 172-173; 175pp; English.
 XX

Query Match	100.0%	Pred. 15.4%	DB 21%	Length 298;
Best Local Similarity	100.0%	Pred. NO. 1.8e-157;		
Matches 298;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MTEQAISEFADKDFLAGIGIAAISKTVAPAPLERKLLLOVHASKIAADKQYKGIYDICTVR	60	
Db	1	mtedqisistakdliagqiaaalskctvapiervkllllyqhnaskqiaadkqykgivdcivr	60	
QY	61	IPKEQGVLSFWRGNLANVIRFFPTQALNFAFKDKKQKQIFLGVDVHDHTQFWRYFAGNLASG	120	
Db	61	ipkegvslsfwrnglanvlyrfptqalnfafdkkykqiflgvdvhdhtqfwryfaagnlasg	120	
QY	121	GAGATFSLCFYVPLDFPARNRLAADVGKSGTEREERGLDCLVYITKSDGIRGLYOGFSVS	180	
Db	121	gaagatslcfyvpldfpartrlaadvgksgterefrgldclvlyitksgdirglyogfsvs	180	
QY	181	VQGIIVYRAATFEGVYDTRAKGMLPDPKKNHHIVYSMMIAQTVRAVAGVSYEPRTVRRKMM	240	
Db	181	vqgiivylraayfygydtrakgmlpdpknchivysmmiaqtlvavagvsyepftrrrmm	240	
QY	241	OSGRKGADIMYGTVDCKNRKTIERDGGKAFKFGAMSANVLRGMGSAFVLYIVDELKKVI	298	
Db	241	qsgirvgadimylvgtvdckwrlfdeggaafkfgamsanvlfmggsafvlyivdelkkvi	298	

CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC dTTP-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT2 from human brain.
xx

SX Sequence 298 AA:

Query Match 94.2%; Score 1454; DB 21; Length 298;
Best Local Similarity 92.6%; Pred. NO. 6,5e+18;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

RESULT	2
ID	Y71032
XX	Y71032 standard; Protein; 298 AA.
AC	
XX	Y71032;
DT	29-AUG-2000 (first entry)
XX	
DE	Human adenine nucleotide translocator ANT2.
XX	
KW	Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer
KW	mitochondrial permeability transition; neuroprotective; noctropic;
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW	antiparasitic; cerebroprotective; therapeutic; screening; psoriasis;

Dd	1	mtdaalsfakckflaggvaaaastkavpieriervkllllqyqphaskfitedckqkxgllidcivr	60
Oy	61	IPKEGVLSFPMRGMLANVIRYPTQALNFARCKDXKQKQIFLGVDVKHPOFWRYFAGNLASG	120
Dd	61	lpeqevsisfwrcgmlanviryfpcahlfakcdkxkqgflf9gvdkrcqfwyifagnlaag	120
Oy	121	GAACGTSICFYVPPLDFAFTRLAAYVKSCTGERERGGDCLVTKTKSDGIRGLAQGHSVS	180
Dd	121	gaagtsicfcyvppldfatrrlaaadvqkxgaeretf9gdcivtkyksdgl9lylqgfnvs	180
Oy	181	VGGIIYFAAYFGVVDPAKGM.LDPBKNTHIYVSNMIAQOTYAVALGVVSPFDYVRRMM	240
Dd	181	vgglliyfaayfglyldctekgm.lprpbkntihlyismiaqlgvtaavaglcsyprdcvtrrrrmm	240
Oy	241	QSGRRGADIMTYGVDCWRKITRDEGGCAKFFKGAMSNVLRGMGSAFVLLVYLDLKK	296

[illegible]

Oy	121	GAACATCTGCYVPLDPEFRRLADYKSCGSEERFRLGCLVIRKSDGIRSLYGCFSVS	180
Db	121	gaagatcctcvtpldfrtllaaadvkqssqrefnglqcltkkirksglxyglvgfvs	180
Oy	181	VQGIIVRAAYFCGYDTAKGMLDPDKNTHIVYSWMIATQVTVAAGVSYPEDFVRRMM	240
Db	181	vqglllyraayfgyvdtakgmlpdkpnhvlivswwlaagvatavaglvspfdvtrrmm	240
Oy	241	QSGKKAGDIWYTGVCWKRKIFPDEGGKAFPGKGSNVLARGGAFVLVDELKVI	298
Db	241	qsrgkagdiwytgvlcdwrkikdeganaefkxgawsnvlrimgafvlvlydelkkyv	298
RESULT	4		
ID	Y71031	standard; Protein: 297 AA.	
AC	Y71031		
XX	Y71031		
DT	29-AUG-2000	(first entry)	
XX			
DE		Human adenine nucleotide translocator ANT1.	
XX			
KW		Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP;	
KW		adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;	
KW		mitochondrial permeability transition; neuroprotective; nocrotic;	
KW		antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;	
KW		antipariatic; cerebroprotective; therapeutic; screening; psoriasis;	
KW		Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;	
KW		diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;	
KW		mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;	
KW		mitochondrial diabetes and deafness; hyperproliferative disorder;	
KW		myoclonic epilepsy red ragged fibre syndrome.	
XX			
OS		Homo sapiens.	
XX			
PN		MO200026370-A2.	
PD		11-MAY-2000.	
XX			
PF		03-NOV-1999; 99MO-US25883.	
XX			
XX		03-NOV-1998; 98US-0185904.	
PR		08-SEP-1999; 99US-0393441.	
XX			
PA		(MITO-) MITOKOR.	
P1		Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;	
P1		Ghosh SS;	
DR		N-PSDB: D00519.	
XX			
XX		WPI: 2000-365619/31.	
PT			
PT		Recombinant construct encoding adenine nucleotide translocator	
PT		polypeptide, useful e.g. in screening for potential therapeutic agents	
XX		against mitochondrial disease	
PS		Claim 44: Page 172: 175pp: English.	
XX			
CC		The patent discloses a method to produce adenine nucleotide translocator	
CC		(ANT) proteins or ANT fusion proteins using recombinant expression	
CC		constructs. ANT is a nuclear encoded protein and a major component of	
CC		inner mitochondrial membrane. It mediates transport of adenosine	
CC		di/tri-phosphates across the mitochondrial inner membrane and also serves	
CC		as an important molecular component of the mitochondrial permeability	
CC		transition pore, a modulator of apoptosis. ANT is used to identify agents	
CC		or ligands that bind to, or interact with it. The ANT ligands are used to	
CC		detect or isolate ANT in a biological sample, and therapeutically for	
CC		regulating mitochondrial pore activity, for treating diseases associated	
CC		with altered mitochondrial function, including Alzheimer's, Parkinson's	
CC		and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,	
CC		Leber's hereditary optic neuropathy, schizophrenia, mitochondrial	

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PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
PR 08-APR-1999; 9905-0128714.
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PR 28-OCT-1999; 99US-0161992.
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Query Match 48.1%; Score 742.5; DB 21; Length 346;
Best Local Similarity 52.8%; Pred. No. 2e-71;
Matches 160; Conservative 45; Mismatches 77; Indels 21; Gaps 7;

OY 7 SFADPLAGAGIAAISTATAPIRNVKLLQVHASKOIAA---DKOYKGVDCIVRPK 63
DB 44 nfaIdfmgysaaavsktaaplerkvlllqnq--demikagrlsepyksgdcfgtrtlk 101
OY 64 EOGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVNDKHQFNRYPAGNLASGAA 123
DB 102 deqfsgslvrgntanviryfptqalnfaifkdyfkrllfnfkdr-dgykwvfagnlasgaa 160
OY 124 GANSLCFVPLDEAFARLAD---VGKSGTEREERGLGDLCLVKTGSDGIRGLYQGESVS 180
DB 161 gasallfvyldyartclandakaakkgyggrqfdglvdyrfcltkcdglaglyrgfnls 220
OY 181 VQGIIRRAAYFGVYDPAK-----GMLPDKNTIIVSWMTAQVTVAVAGVSTPEPTVR 235
DB 221 cvglivryrglyfglydsvkpylllgdldqdsffasfalgwvl---tnqaqlasypldctvr 276
OY 236 RRMWOGSRKGADIMYGTVCWRKIFRDEGKAFKFGAMSNVLRGMGAFVLVLYDELK 295
DB 277 rrmmttgea---vkyslsdafkqllknegaslkfkgaganlltrvagagvlsygdldq 333
OY 296 KVI 298
DB 334 ltv 336
RESULT 7
G37264
ID G37264 standard; Protein; 346 AA.
XX
AC G37264;
XX
DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 45792.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX

OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
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PE 25-FEB-2000; 2000EP-0301439.
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Query Match	48.1%	Score 742.5	DB 21	Length 346
Best Local Similarity	52.8%	Pred. No. 2e-71		
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Db	44	nfaIdfImgySaavsktaaaPierVKllIInq--demIkagrlsepykIgiGdfGrtIk	100
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Oy	124	GATSCAFYVYPLDPMRTRIAAD---VGSAGTEREERGIGDCLVKTfKSDGfRGVLQGSVS	180
Db	161	gassllfYasIdyatrclIandakaakfyggagIdglVdyrKtLtkCtgaIaglyrGfInIs	220
Oy	181	VOGIIYRAAFEGVYDTAK---GMLPDPKNTHIIVVSMMLIAQTVTVAAGVSYPFDTVR	235
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Oy	236	RRMMOSGRKADIMYGTVCWCKIRfRDECGKfFfGAMSVNVRGNGGAFVLVLVDELK	295
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		: :	
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AC G38460;
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DT 18-OCT-2000 (first entry)
XX
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
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XX
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PF 25-FEB-2000; 2000EP-0301439.
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Query Match 48.1%; Score 742.5; DB 21; Length 346;
Best Local Similarity 52.8%; Pred. No. 2e-71;
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OY 124 GATSLCFVYPADFAFTRIAAD---VGKSGTEREFGGLDCLVKITKSGIGLYOGFSES 180
DB 161 gasslllfytsldyartclandakaakkggggrgfdglvdyrklclktcdgaglyrgfnis 220
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AC G36576;
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KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
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Query Match 48.18; Score 742.5; DB 21; Length 363;
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XX AC G37260;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 45787.
XX KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX OS
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000: 2000EP-0301439.
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Query Match	48.1%;	Score 742.5;	DB 21;	Length 363;
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OY	124	GATSLCEFYPLDPRKTRLAAD---VGSSEGEREREGIDCLVKITKSDGIRGLYGFSSVS	180
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OY	181	VOGIIIEAAAFEGVYDPAK-----GMLEDDPKNTHIVSWMIAGQVTVAVAGVSYPEPTVR	235
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OY	236	RRMMQSGRKAGADIMYTGVDQMKRIERDESGKAFKFGANSNVLRGNGCAFVVLVDELK	295
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DT	18-OCT-2000 (first entry)		
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 44843.		

XX Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay: genetic mapping; gene expression control; promoter;
KM termination sequence.
XX Arabidopsis thaliana.
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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DB 137 degfsgIwrgtanlvtyrfpqalnfafkdyfkrIlnfkdxr-dgykwkfaglnasgaa 195
OY 124 GATSLCAVYELDFKATRLAAD---VGKSGTERERKGLDCLVKTKSDGIRGLYQGSVS 180
DB 196 gasellIvlyldyartIandakaakkg99rgfdgIvdYrklclkdglagIyrgfnIs 255
OY 181 VOGIIIRAAVFGVYDPAK-----GMLPDPKNTIIVSMWIAQVTVAVAGVSVPEPTVR 235
DB 256 cvglIvYrgIyfgIydvskvpllIqdlqdsIfasfaIgwI----tngagIasypIdctvr 311
OY 236 RRMAMOSGRGADIMYGTGDCMRKIFRDEGKAFFKAWSNVLRGCGAFVLVYDELK 295
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DB 369 liv 371
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KW termination sequence.
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KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
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